#### SEQUENCE LISTING

- (1) GENERAL INFORMATION:
  - (i) APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
- (ii) TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and Uses Therefor
  - (iii) NUMBER OF SEQUENCES: 23
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: Genentech, Inc.
    - (B) STREET: 1 DNA Way
    - (C) CITY: South San Francisco
    - (D) STATE: California
    - (E) COUNTRY: USA
    - (F) ZIP: 94080
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: WinPatin (Genentech)
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER:
    - (B) FILING DATE: 11-Jan-2000
    - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/899,437
  - (B) FILING DATE: 07/24/1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Conley, Deirdre L.
  - (B) REGISTRATION NUMBER: 36,487
  - (C) REFERENCE/DOCKET NUMBER: P1084R1C1
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: 650/225-2066
    - (B) TELEFAX: 650/952-9881
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2538 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: mouse NRG3 nucleic acid
  - (B) LOCATION: 1-2538
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGACCGGC	CGGCGGCGCC	CGGGCCGGTC	TCGCCCCTCT	ACCGAGCGCC	50
TCGCCGCCCC	CTCCCGGCC	CGCGTCCCCT	CCCCCGTCCT	CTCCTCCCCG	100
cccgccgccc	GCCTCTCGGG	GGGAGGGGCG	TGGGGGCAGG	GAGCCGATTT	150
GCATGCGGCC	GCCGCGGCCG	CTGCCTGAGC	CGGAGCCCGC	CGCCGCCGGA	200
GCCCGCGCCC	GCGCCCGCGC	ccgcccccc	CGGCCCCATG	CCTCTGGCGC	250
GGCCCTCGGG	GGGGCGAAGG	TGAAGATCGG	CTCCTAGGAT	GAGTGAAGGG	300
GCGGCCGGTG	CCTCGCCACC	TGGTGCCGCT	TCGGCAGCCG	CCGCCTCAGC	350
CGAGGAGGGC	ACCGCGGCGG	CTGCGGCGGC	GGCGGCGGCG	GGCGGGGGCC	400
CGGACGGCGG	CGGAGAAGGG	GCGGCCGAAC	CCCCCGGGA	GTTACGCTGT	450
AGCGACTGCA	TCGTGTGGAA	CCGGCAGCAG	ACGTGGTTGT	GCGTGGTGCC	500
TCTGTTCATC	GGCTTCATCG	GCCTGGGGCT	CAGCCTCATG	CTGCTTAAAT	550
GGATCGTGGT	AGGCTCCGTC	AAGGAGTACG	TGCCCACGGA	CCTGGTGGAC	600
TCCAAGGGAA	TGGGCCAGGA	CCCCTTCTTC	CTCTCCAAGC	CCAGCTCTTT	650
CCCCAAGGCT	ATGGAAACCA	CCACAACAAC	CACTTCTACC	ACGTCCCCCG	700
CCACCCCTC	TGCCGGCGGC	GCCGCTTCTT	CCAGGACGCC	TAACCGGATT	750
AGCACCCGCT	TGACCACCAT	CACACGGGCA	CCCACCCGCT	TCCCTGGGCA	800
CCGGGTTCCC	ATCCGGGCTA	GCCCGCGCTC	TACCACAGCA	CGGAACACTG	850
CTGCCCCTCC	GACGGTCCTG	TCCACCACGG	CCCCTTTCTT	CAGTAGCAGC	900
ACGCCCGGCT	CCCGACCCCC	GATGCCAGGA	GCCCCAGTA	CGCAGGCGAT	950
GCCTTCCTGG	CCCACTGCGG	CGTATGCTAC	CTCCTCCTAC	CTCCACGATT	1000
CCACTCCCTC	CTGGACCCTG	TCACCCTTTC	AGGATGCTGC	TGCCGCCTCT	1050
TCCTCCTCAC	CCTCTTCCAC	CTCCTCCACT	ACCACCACCC	CAGAAACTAG	1100
CACCAGCCCC	AAATTTCATA	CTACAACATA	CTCCACTGAA	CGATCTGAGC	1150
ACTTCAAACC	CTGTCGAGAC	AAGGACCTGG	CGTATTGTCT	CAATGATGGT	1200
GAATGCTTTG	TGATTGAGAC	CCTGACAGGA	TCCCATAAGC	ACTGTCGGTG	1250
CAAGGAAGGC	TACCAAGGAG	TCCGTTGTGA	TCAATTTCTG	CCGAAAACAG	1300
ACTCCATCTT	ATCGGATCCA	ACAGACCACT	TGGGGATTGA	ATTCATGGAG	1350
AGTGAAGACG	TTTATCAAAG	GCAGGTGCTG	TCAATTTCAT	GTATCATCTT	1400

TGGAATTGTC ATCGTGGGCA TGTTCTGTGC AGCATTCTAC TTCAAAAGCA 1450 AGAAACAAGC TAAACAAATT CAGGAGCACC TGAAAGAGTC ACAGAATGGG 1500 AAGAACTACA GCCTCAAGGC ATCCAGCACA AAGTCTGAGA GCTTGATGAA 1550 GAGCCATGTC CATCTACAAA ATTATTCAAA GGCGGATAGG CATCCTGTGA 1600 CTGCGCTGGA GAAAATAATG GAGTCAAGTT TTTCAGCTCC CCAGTCGTTC 1650 CCAGAAGTCA CTTCTCCTGA CCGAGGAAGC CAGCCTATCA AGCACCACAG 1700 CCCAGGACAA AGGAGTGGGA TGTTGCATAG GAATACTTTC AGAAGGGCAC 1750 CACCCTCACC CCGAAGTCGA CTGGGTGGTA TTGTAGGACC AGCATATCAA 1800 GATAGAGGTC AGGAAGACTA TATCCCACCT GCCTATACAG CTGTGGTGTG 1900 TTGAAAGACC CCTGGACTTA AAGTATGTGT CCAATGGCTT AAGAACCCAA 1950 CAAAATGCAT CAATAAATAT GCAACTGCCT TCAAGAGAGA CAAACCCCTA 2000 TTTTAATAGC TTGGATCAAA AGGACCTGGT GGGTTATTTA TCCCCAAGGG 2050 CCAATTCTGT GCCCATCATC CCGTCGATGG GTCTAGAAGA AACCTGCATG 2100 CAAATGCCAG GGATTTCTGA CGTCAAAAGC ATTAAATGGT GCAAAAACTC 2150 CTACTCCGCT GACATTGTCA ACGCGAGTAT GCCAGTCAGT GATTGTCTTC 2200 TAGAAGAACA ACAGGAAGTG AAAATATTAC TAGAGACTGT GCAGGAACAG 2250 ATCCGGATTC TGACTGATGC CAGACGGTCA GAAGACTTCG AACTGGCCAG 2300 CATGGAAACT GAGGACAGTG CGAGCGAAAA CACAGCCTTT CTCCCCCTGA 2350 GTCCCACGGC CAAATCAGAA CGAGAGGCAC AATTTGTCTT AAGAAATGAA 2400 ATACAAAGAG ACTCTGTGCT AACCAAGTGA CTGGAAATGT AGGAATCTGT 2450 GCATTATATG CTTTGCTAAA CAGGAAGGAG AGGAAATTAA ATACAAATTA 2500 TTTATATGCA TTAATTTAAG AGCATCTACT TAGAAGCC 2538

#### (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 713 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

## (ix) FEATURE:

- (A) NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
- (B) LOCATION: 1-713
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met 1	Ser	Glu	Gly	Ala 5	Ala	Gly	Ala	Ser	Pro 10	Pro	Gly	Ala	Ala	Ser 15
Ala	Ala	Ala	Ala	Ser 20	Ala	Glu	Glu	Gly	Thr 25	Ala	Ala	Ala	Ala	Ala 30
Ala	Ala	Ala	Ala	Gly 35	Gly	Gly	Pro	Asp	Gly 40	Gly	Gly	Glu	Gly	Ala 45
Ala	Glu	Pro	Pro	Arg 50	Glu	Leu	Arg	Cys	Ser 55	Asp	Cys	Ile	Val	Trp 60
Asn	Arg	Gln	Gln	Thr 65	Trp	Leu	Cys	Val	Val 70	Pro	Leu	Phe	Ile	Gly 75
Phe	Ile	Gly	Leu	Gly 80	Leu	Ser	Leu	Met	Leu 85	Leu	Lys	Trp	Ile	Val 90
Val	Gly	Ser	Val	Lys 95	Glu	Tyr	Val	Pro	Thr 100	Asp	Leu	Val	Asp	Ser 105
Lys	Gly	Met	Gly	Gln 110	Asp	Pro	Phe	Phe	Leu 115	Ser	Lys	Pro	Ser	Ser 120
Phe	Pro	Lys	Ala	Met 125	Glu	Thr	Thr	Thr	Thr 130	Thr	Thr	Ser	Thr	Thr 135
Ser	Pro	Ala	Thr	Pro 140	Ser	Ala	Gly	Gly	Ala 145	Ala	Ser	Ser	Arg	Thr 150
Pro	Asn	Arg	Ile	Ser 155	Thr	Arg	Leu	Thr	Thr 160	Ile	Thr	Arg	Ala	Pro 165
Thr	Arg	Phe	Pro	Gly 170	His	Arg	Val	Pro	Ile 175	Arg	Ala	Ser	Pro	Arg 180
Ser	Thr	Thr	Ala	Arg 185	Asn	Thr	Ala	Ala	Pro 190	Pro	Thr	Val	Leu	Ser 195
Thr	Thr	Ala	Pro	Phe 200	Phe	Ser	Ser	Ser	Thr 205	Pro	Gly	Ser	Arg	Pro 210
Pro	Met	Pro	Gly	Ala 215	Pro	Ser	Thr	Gln	Ala 220	Met	Pro	Ser	Trp	Pro 225
Thr	Ala	Ala	Tyr	Ala 230	Thr	Ser	Ser	Tyr	Leu 235	His	Asp	Ser	Thr	Pro 240
Ser	Trp	Thr	Leu	Ser 245	Pro	Phe	Gln	Asp	Ala 250	Ala	Ala	Ala	Ser	Ser 255
Ser	Ser	Pro	Ser	Ser 260	Thr	Ser	Ser	Thr	Thr 265	Thr	Thr	Pro	Glu	Thr 270
Ser	Thr	Ser	Pro	Lys 275	Phe	His	Thr	Thr	Thr 280	Tyr	Ser	Thr	Glu	Arg 285

Ser	Glu	His	Phe	Lys 290	Pro	Суѕ	Arg	Asp	Lys 295	Asp	Leu	Ala	Tyr	Cys 300
Leu	Asn	Asp	Gly	Glu 305	Суѕ	Phe	Val	Ile	Glu 310	Thr	Leu	Thr	Gly	Ser 315
His	Lys	His	Cys	Arg 320	Суѕ	Lys	Glu	Gly	Tyr 325	Gln	Gly	Val	Arg	Cys 330
Asp	Gln	Phe	Leu	Pro 335	Lys	Thr	Asp	Ser	Ile 340	Leu	Ser	Asp	Pro	Thr 345
Asp	His	Leu	Gly	Ile 350	Glu	Phe	Met	Glu	Ser 355	Glu	Asp	Val	Tyr	Gln 360
Arg	Gln	Val	Leu	Ser 365	Ile	Ser	Суѕ	Ile	Ile 370	Phe	Gly	Ile	Val	Ile 375
Val	Gly	Met	Phe	Cys 380	Ala	Ala	Phe	Tyr	Phe 385	Lys	Ser	Lys	Lys	Gln 390
Ala	Lys	Gln	Ile	Gln 395	Glu	His	Leu	Lys	Glu 400	Ser	Gln	Asn	Gly	Lys 405
Asn	Tyr	Ser	Leu	Lys 410	Ala	Ser	Ser	Thr	Lys 415	Ser	Glu	Ser	Leu	Met 420
Lys	Ser	His	Val	His 425	Leu	Gln	Asn	Tyr	Ser 430	Lys	Ala	Asp	Arg	His 435
Pro	Val	Thr	Ala	Leu 440	Glu	Lys	Ile	Met	Glu 445	Ser	Ser	Phe	Ser	Ala 450
Pro	Gln	Ser	Phe	Pro 4.55	Glu	Val	Thr	Ser	Pro 460	Asp	Arg	Gly	Ser	Gln 465
Pro	Ile	Lys	His	His 470	Ser	Pro	Gly	Gln	Arg 475	Ser	Gly	Met	Leu	His 480
Arg	Asn	Thr	Phe	Arg 485	Arg	Ala	Pro	Pro	Ser 490	Pro	Arg	Ser	Arg	Leu 495
Gly	Gly	Ile	Val	Gly 500	Pro	Ala	Tyr	Gln	Gln 505	Leu	Glu	Glu	Ser	Arg 510
Ile	Pro	Asp	Gln	Asp 515	Thr	Ile	Pro	Cys	Gln 520	Gly	Ile	Glu	Val	Arg 525
Lys	Thr	Ile	Ser	His 530	Leu	Pro	Ile	Gln	Leu 535	Trp	Cys	Val	Glu	Arg 540
Pro	Leu	Asp	Leu	Lys 545	Tyr	Val	Ser	Asn	Gly 550	Leu	Arg	Thr	Gln	Gln 555
Asn	Ala	Ser	Ile	Asn 560	Met	Gln	Leu	Pro	Ser 565	Arg	Glu	Thr	Asn	Pro 570

Tyr	Phe	Asn	Ser	Leu 575	Asp	Gln	Lys	Asp	Leu 580	Val	Gly	Tyr	Leu	Ser 585
Pro	Arg	Ala	Asn	Ser 590	Val	Pro	Ile	Ile	Pro 595	Ser	Met	Gly	Leu	Glu 600
Glu	Thr	Cys <sup>,</sup>	Met	Gln 605	Met	Pro	Gly	Ile	Ser 610	Asp	Val	Lys	Ser	Ile 615
Lys	Trp	Суѕ	Lys	Asn 620	Ser	Tyr	Ser	Ala	Asp 625	Ile	Val	Asn	Ala	Ser 630
Met	Pro	Val	Ser	Asp 635	Cys	Leu	Leu	Glu	Glu 640	Gln	Gln	Glu	Val	Lys 645
Ile	Leu	Leu	Glu	Thr 650	Val	Gln	Glu	Gln	Ile 655	Arg	Ile	Leu	Thr	Asp 660
Ala	Arg	Arg	Ser	Glu 665	Asp	Phe	Glu	Leu	Ala 670	Ser	Met	Glu	Thr	Glu 675
Asp	Ser	Ala	Ser	Glu 680	Asn	Thr	Ala	Phe	Leu 685	Pro	Leu	Ser	Pro	Thr 690
Ala	Lys	Ser	Glu	Arg 695	Glu	Ala	Gln	Phe	Val 700	Leu	Arg	Asn	Glu	Ile 705
Gln	Arg	Asp	Ser	Val	Leu	Thr	Lys							

# (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 362 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

#### (ix) FEATURE:

- (A) NAME/KEY: mNRG3 extracellular domainAmino acid seq
- (B) LOCATION: 1-362
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Glu Gly Ala Ala Gly Ala Ser Pro Pro Gly Ala Ala Ser 1 5 10 15

Ala Ala Ala Gly Gly Gly Pro Asp Gly Gly Gly Glu Gly Ala 35 40 . 45

Ala Glu Pro Pro Arg Glu Leu Arg Cys Ser Asp Cys Ile Val Trp 50 55 60

Asn Arg Gln Gln Thr Trp Leu Cys Val Val Pro Leu Phe Ile Gly Phe Ile Gly Leu Gly Leu Ser Leu Met Leu Leu Lys Trp Ile Val Val Gly Ser Val Lys Glu Tyr Val Pro Thr Asp Leu Val Asp Ser Lys Gly Met Gly Gln Asp Pro Phe Phe Leu Ser Lys Pro Ser Ser 115 Phe Pro Lys Ala Met Glu Thr Thr Thr Thr Thr Thr Ser Thr Thr 130 135 Ser Pro Ala Thr Pro Ser Ala Gly Gly Ala Ala Ser Ser Arg Thr 145 Pro Asn Arg Ile Ser Thr Arg Leu Thr Thr Ile Thr Arg Ala Pro 160 Thr Arg Phe Pro Gly His Arg Val Pro Ile Arg Ala Ser Pro Arg Ser Thr Thr Ala Arg Asn Thr Ala Ala Pro Pro Thr Val Leu Ser 195 190 Thr Thr Ala Pro Phe Phe Ser Ser Ser Thr Pro Gly Ser Arg Pro 205 Pro Met Pro Gly Ala Pro Ser Thr Gln Ala Met Pro Ser Trp Pro 220 Thr Ala Ala Tyr Ala Thr Ser Ser Tyr Leu His Asp Ser Thr Pro Ser Trp Thr Leu Ser Pro Phe Gln Asp Ala Ala Ala Ser Ser 250 255 Ser Ser Pro Ser Ser Thr Ser Ser Thr Thr Thr Pro Glu Thr Ser Thr Ser Pro Lys Phe His Thr Thr Thr Tyr Ser Thr Glu Arg 280 285 Ser Glu His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys Leu Asn Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser 305 His Lys His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys Asp Gln Phe Leu Pro Lys Thr Asp Ser Ile Leu Ser Asp Pro Thr 335

Asp His Leu Gly Ile Glu Phe Met Glu Ser Glu Asp Val Tyr Gln 350 355 360

Arg Gln 362

- (2) INFORMATION FOR SEQ ID NO:4:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 47 amino acids
    - (B) TYPE: Amino Acid
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: NRG3 EGF-like domain/amino acid seq.
  - (B) LOCATION: 1-47
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys Leu Asn 1 5 10 15

Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser His Lys 20 25 30

His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys Asp Gln 35 40 45

Phe Leu 47

- (2) INFORMATION FOR SEQ ID NO:5:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2502 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: Human NRG3B1(hNRG3B1)/nucleic acid seq.
  - (B) LOCATION: 1-2502
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCACCGACCT AGTGGACTCC ACTAGGTCGG TGGGCACGTA CTCCTTGACG 50
GAGCCCACCA CGATCCATTT GAGAAGCATG AGGCGCGGCC CCATGCCTCT 100
GCCGCGGCCC TCGGGGGGC GAAGGTGAAN ACCGGCTCCT AGGATGAGTG 150
AAGGGGCGGC CGCTGCCTCG CCACCTGGTG CCGCTTCGGC AGCCGCCGCC 200

TCGGCCGAGG AGGGCACCGC GGCGGCTGCG GCGGCGGCAG CGGCGGGCGG 250 GGGCCCGGAC GGCGCCGCG AAGGGGCCGCC CGGGAGTTAC 300 GCTGTAGCGA CTGCATCGTG TGGAACCGGC AGCAGACGTG GCTGTGCGTG 350 GTACCTCTGT TCATCGGCTT CATCGGCCTG GGGCTCAGCC TCATGCTTCT 400 CAAATGGATC GTGGTGGGCT CCGTCAAGGA GTACGTGCCC ACCGACCTAG 450 TGGACTCCAA GGGGATGGGC CAGGACCCCT TCTTCCTCTC CAAGCCCAGC 500 TCTTTCCCCA AGGCCATGGA GACCACCACC ACTACCACTT CCACCACGTC 550 CCCCGCCACC CCCTCCGCCG GGGGTGCCGC CTCCTCCAGG ACGCCCAACC 600 GGATTAGCAC TCGCCTGACC ACCATCACGC GGGCGCCCAC TCGCTTCCCC 650 GGGCACCGGG TGCCCATCCG GGCCAGCCCG CGCTCCACCA CAGCACGGAA 700 CACTGCGGCC CCTGCGACGG TCCCGTCCAC CACGGCCCCG TTCTTCAGTA 750 GCAGCACGCT GGGCTCCCGA CCCCCGGTGC CAGGAACTCC AAGTACCCAG 800 GCAATGCCCT CCTGGCCTAC TGCGGCATAC GCTACCTCCT CCTACCTTCA 850 CGATTCTACT CCCTCCTGGA CCCTGTCTCC CTTTCAGGAT GCTGCCTCCT 900 CTTCTTCCTC TCCGCTACCA CCACCACAC AGAAACTAGC 950 ACCAGCCCA AATTTCATAC GACGACATAT TCCACAGAGC GATCCGAGCA 1000 CTTCAAACCC TGCCGAGACA AGGACCTTGC ATACTGTCTC AATGATGGCG 1050 AGTGCTTTGT GATCGAAACC CTGACCGGAT CCCATAAACA CTGTCGGTGC 1100 AAAGAAGGCT ACCAAGGAGT CCGTTGTGAT CAATTTCTGC CGAAAACTGA 1150 TTCCATCTTA TCGGATCCAA CAGACCACTT GGGGATTGAA TTCATGGAGA 1200 GTGAAGAAGT TTATCAAAGG CAGGTGCTGT CAATTTCATG TATCATCTTT 1250 GGAATTGTCA TCGTGGGCAT GTTCTGTGCA GCATTCTACT TCAAAAGCAA 1300 GAAACAAGCT AAACAAATCC AAGAGCAGCT GAAAGTGCCA CAAAATGGTA 1350 AAAGCTACAG TCTCAAAGCA TCCAGCACAA TGGCAAAGTC AGAGAACTTG 1400 GTGAAGAGCC ATGTCCAGCT GCAAAATTAT TCAAAGGTGG AAAGGCATCC 1450 TGTGACTGCA TTGGAGAAAA TGATGGAGTC AAGTTTTGTC GGCCCCCAGT 1500 CATTCCCTGA GGTCCCTTCT CCTGACAGAG GAAGCCAGTC TGTCAAACAC 1550 CACAGGAGTC TATCCTCTTG CTGCAGCCCA GGGCAAAGAA GTGGCATGCT 1600 CCATAGGAAT GCCTTCAGAA GGACACCCCC GTCACCCCGA AGTAGGCTAG 1650

GTGGAATTGT GGGACCAGCA TATCAGCAAC TCGAAGAATC AAGGATCCCA 1700 GACCAGGATA CGATACCTTG CCAAGGGATA GAGGTCAGGA AGACTATATC 1750 CCACCTGCCT ATACAGCTGT GGTGTGTTGA AAGACCCCTG GACTTAAAGT 1800 ATTCATCCAG TGGTTTAAAA ACCCAACGAA ATACATCAAT AAATATGCAA 1850 CTGCCTTCAA GAGAGACAAA CCCCTATTTT AATAGCTTGG AGCAAAAGGA 1900 CCTGGTGGGC TATTCATCCA CAAGGGCCAG TTCTGTGCCC ATCATCCCTT 1950 CAGTGGGTTT AGAGGAAACC TGCCTGCAAA TGCCAGGGAT TTCTGAAGTC 2000 AAAAGCATCA AATGGTGCAA AAACTCCTAT TCAGCTGACG TTGTCAATGT 2050 GAGTATTCCA GTCAGCGATT GTCTTATAGC AGAACAACAA GAAGTGAAAA 2100 TATTGCTAGA AACTGTCCAG GAGCAGATCC GAATTCTGAC TGATGCCAGA 2150 CGGTCAGAAG ACTACGAACT GGCCAGCGTA GAAACCGAGG ACAGTGCAAG 2200 CGAAAACACA GCCTTTCTCC CCCTGAGTCC CACAGCCAAA TCAGAACGAG 2250 AGGCGCAATT TGTCTTAAGA AATGAAATAC AAAGAGACTC TGCATTGACC 2300 AAGTGACTTG AGATGTAGGA ATCTGTGCAT TCTATGCTTT GCTCAACAGG 2350 AAAGAGAGGA AATCAAATAC AAATTATTTA TATGCATTAA TTTAAGAGCA 2400 TCTACTTAGA AGAAACCAAA TAGTCTATCG CCCTCATATC ATAGTGTTTT 2450 TTAACAAAAT ATTTTTTAA GGGAAAGAAA TGTTTCAGGA GGGATAAAGC 2500 TT 2502

- (2) INFORMATION FOR SEQ ID NO:6:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 720 amino acids
    - (B) TYPE: Amino Acid
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: hNRG3B1 amino acid sequence
  - (B) LOCATION: 1-720
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Glu Gly Ala Ala Ala Ala Ser Pro Pro Gly Ala Ala Ser 1 5 10 15

Ala Ala Ala Ser Ala Glu Glu Gly Thr Ala Ala Ala Ala Ala 20 25 30

Ala Ala Ala Gly Gly Gly Pro Asp Gly Gly Glu Gly Ala Ala Glu Pro Pro Arg Glu Leu Arg Cys Ser Asp Cys Ile Val Trp Asn Arg Gln Gln Thr Trp Leu Cys Val Val Pro Leu Phe Ile Gly Phe Ile Gly Leu Gly Leu Ser Leu Met Leu Leu Lys Trp Ile Val Val Gly Ser Val Lys Glu Tyr Val Pro Thr Asp Leu Val Asp Ser Lys Gly Met Gly Gln Asp Pro Phe Phe Leu Ser Lys Pro Ser Ser 115 Phe Pro Lys Ala Met Glu Thr Thr Thr Thr Thr Thr Ser Thr Thr Ser Pro Ala Thr Pro Ser Ala Gly Gly Ala Ala Ser Ser Arg Thr Pro Asn Arg Ile Ser Thr Arg Leu Thr Thr Ile Thr Arg Ala Pro Thr Arg Phe Pro Gly His Arg Val Pro Ile Arg Ala Ser Pro Arg Ser Thr Thr Ala Arg Asn Thr Ala Ala Pro Ala Thr Val Pro Ser Thr Thr Ala Pro Phe Phe Ser Ser Thr Leu Gly Ser Arg Pro Pro Val Pro Gly Thr Pro Ser Thr Gln Ala Met Pro Ser Trp Pro Thr Ala Ala Tyr Ala Thr Ser Ser Tyr Leu His Asp Ser Thr Pro Ser Trp Thr Leu Ser Pro Phe Gln Asp Ala Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ala Thr Thr Thr Pro Glu Thr Ser Thr Ser Pro Lys Phe His Thr Thr Tyr Ser Thr Glu Arg Ser Glu 275 His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys Leu Asn 295 Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser His Lys 305 310 315

His	Cys	Arg	Cys	Lys 320	Glu	Gly	Tyr	Gln	Gly 325	Val	Arg	Cys	Asp	Gln 330
Phe	Leu	Pro	Lys	Thr 335	Asp	Ser	Ile	Leu	Ser 340	Asp	Pro	Thr	Asp	His 345
Leu	Gly	Ile	Glu	Phe 350	Met	Glu	Ser	Glu	Glu 355	Val	Tyr	Gln	Arg	Gln 360
Val	Leu	Ser	Ile	Ser 365	Суѕ	Ile	Ile	Phe	Gly 370	Ile	Val	Ile	Val	Gly 375
Met	Phe	Cys	Ala	Ala 380	Phe	Tyr	Phe	Lys	Ser 385	Lys	Lys	Gln	Ala	Lys 390
Gln	Ile	Gln	Glu	Gln 395	Leu	Lys	Val	Pro	Gln 400	Asn	Gly	Lys	Ser	Tyr 405
Ser	Leu	Lys	Ala	Ser 410	Ser	Thr	Met	Ala	Lys 415	Ser	Glu	Asn	Leu	Val 420
Lys	Ser	His	Val	Gln 425	Leu	Gln	Asn	Tyr	Ser 430	Lys	Val	Glu	Arg	His 435
Pro	Val	Thr	Ala	Leu 440	Glu	Lys	Met	Met	Glu 445	Ser	Ser	Phe	Val	Gly 450
Pro	Gln	Ser	Phe	Pro 455	Glu	Val	Pro	Ser	Pro 460	Asp	Arg	Gly	Ser	Gln 465
Ser	Val	Lys	His	His 470	Arg	Ser	Leu	Ser	Ser 475	Cys	Cys	Ser	Pro	Gly 480
Gln	Arg	Ser	Gly	Met 485	Leu	His	Arg	Asn	Ala 490	Phe	Arg	Arg	Thr	Pro 495
Pro	Ser	Pro	Arg	Ser 500	Arg	Leu	Gly	Gly	Ile 505	Val	Gly	Pro	Ala	Tyr 510
Gln	Gln	Leu	Glu	Glu 515	Ser	Arg	Ile	Pro	Asp 520	Gln	Asp	Thr	Ile	Pro 525
Cys	Gln	Gly	Ile	Glu 530	Val	Arg	Lys	Thr	Ile 535	Ser	His	Leu	Pro	Ile 540
Gln	Leu	Trp	Cys	Val 545	Glu	Arg	Pro	Leu	Asp 550	Leu	Lys	Tyr	Ser	Ser 555
Ser	Gly	Leu	Lys	Thr 560	Gln	Arg	Asn	Thr	Ser 565	Ile	Asn	Met	Gln	Leu 570
Pro	Ser	Arg	Glu	Thr 575	Asn	Pro	Tyr	Phe	Asn 580	Ser	Leu	Glu	Gln	Lys 585
Asp	Leu	Val	Gly	Tyr 590	Ser	Ser	Thr	Arg	Ala 595	Ser	Ser	Val	Pro	Ile 600

Ile	Pro	Ser	Val	Gly 605	Leu	Glu	Glu	Thr	Cys 610	Leu	Gln	Met	Pro	Gly 615
Ile	Ser	Glu	Val	Lys 620	Ser	Ile	Lys	Trp	Cys 625	Lys	Asn	Ser	Tyr	Ser 630
Ala	Asp	Val	Val	Asn 635	Val	Ser	Ile	Pro	Val 640	Ser	Asp	Cys	Leu	Ile 645
Ala	Glu	Gln	Gln	Glu 650	Val	Lys	Ile	Leu	Leu 655	Glu	Thr	Val	Gln	Glu 660
Gln	Ile	Arg	Ile	Leu 665	Thr	Asp	Ala	Arg	Arg 670	Ser	Glu	Asp	Tyr	Glu 675
Leu	Ala	Ser	Val	Glu 680	Thr	Glu	Asp	Ser	Ala 685	Ser	Glu	Asn	Thr	Ala 690
Phe	Leu	Pro	Leu	Ser 695	Pro	Thr	Ala	Lys	Ser 700	Glu	Arg	Glu	Ala	Gln 705
Dho	U a l	LON	Λrα	7 cn	Glu	Tla	Gln	Ara	Aen	Sar	Δla	T.611	Thr	Lvs

## (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

710

- (A) LENGTH: 360 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

## (ix) FEATURE:

(A) NAME/KEY: hNRG3 extracellular domain/Amino AcidSeq

715

720

- (B) LOCATION: 1-360
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Glu Gly Ala Ala Ala Ala Ser Pro Pro Gly Ala Ala Ser 1 . 5 10 15

Ala Ala Ala Ser Ala Glu Glu Gly Thr Ala Ala Ala Ala Ala 20 25 30

Ala Ala Ala Gly Gly Gly Pro Asp Gly Gly Gly Gly Ala 35 40 45

Ala Glu Pro Pro Arg Glu Leu Arg Cys Ser Asp Cys Ile Val Trp 50 55 60

Asn Arg Gln Gln Thr Trp Leu Cys Val Val Pro Leu Phe Ile Gly 65 70 75

Phe Ile Gly Leu Gly Leu Ser Leu Met Leu Leu Lys Trp Ile Val $80 \\ 85 \\ 90$ 

Val Gly Ser Val Lys Glu Tyr Val Pro Thr Asp Leu Val Asp Ser Lys Gly Met Gly Gln Asp Pro Phe Phe Leu Ser Lys Pro Ser Ser 110 115 Phe Pro Lys Ala Met Glu Thr Thr Thr Thr Thr Ser Thr Thr 125 130 Ser Pro Ala Thr Pro Ser Ala Gly Gly Ala Ala Ser Ser Arg Thr Pro Asn Arg Ile Ser Thr Arg Leu Thr Thr Ile Thr Arg Ala Pro Thr Arg Phe Pro Gly His Arg Val Pro Ile Arg Ala Ser Pro Arg Ser Thr Thr Ala Arg Asn Thr Ala Ala Pro Ala Thr Val Pro Ser Thr Thr Ala Pro Phe Phe Ser Ser Ser Thr Leu Gly Ser Arg Pro Pro Val Pro Gly Thr Pro Ser Thr Gln Ala Met Pro Ser Trp Pro 220 Thr Ala Ala Tyr Ala Thr Ser Ser Tyr Leu His Asp Ser Thr Pro Ser Trp Thr Leu Ser Pro Phe Gln Asp Ala Ala Ser Ser Ser 250 Ser Ser Ser Ser Ala Thr Thr Thr Pro Glu Thr Ser Thr Ser Pro Lys Phe His Thr Thr Thr Tyr Ser Thr Glu Arg Ser Glu His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys Leu Asn Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser His Lys 310 315 His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys Asp Gln Phe Leu Pro Lys Thr Asp Ser Ile Leu Ser Asp Pro Thr Asp His 340 345 Leu Gly Ile Glu Phe Met Glu Ser Glu Glu Val Tyr Gln Arg Gln 350 355

#### (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEOUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: NRG3 EGF-like domain/amino acid seq.
  - (B) LOCATION: 1-47
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys Leu Asn .1 5 10 15

Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser His Lys
20 25 30

His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys Asp Gln 35 40 45

Phe Leu

47

- (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 48 amino acids
    - (B) TYPE: Amino Acid
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: cARIA.egf
  - (B) LOCATION: 1-48
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

His Leu Thr Lys Cys Asp Ile Lys Gln Lys Ala Phe Cys Val Asn
1 5 10 15

Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro Asn Pro Pro Arg 20 25 30

Tyr Leu Cys Arg Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln 35 40 45

Asn Tyr Val

48

- (2) INFORMATION FOR SEQ ID NO:10:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 45 amino acids
    - (B) TYPE: Amino Acid
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: hAR.egf
  - (B) LOCATION: 1-45
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Lys Asn Pro Cys Asn Ala Glu Phe Gln Asn Phe Cys Ile His
1 5 10 15

Gly Glu Cys Lys Tyr Ile Glu His Leu Glu Ala Val Thr Cys Lys
20 25 30

Cys Gln Gln Glu Tyr Phe Gly Glu Arg Cys Gly Glu Lys Ser Met
35 40 45

- (2) INFORMATION FOR SEQ ID NO:11:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 45 amino acids
    - (B) TYPE: Amino Acid
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: hBTC.efg
  - (B) LOCATION: 1-45
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

His Phe Ser Arg Cys Pro Lys Gln Tyr Lys His Tyr Cys Ile Lys
1 10 15

Gly Arg Cys Arg Phe Val Val Ala Glu Gln Thr Pro Ser Cys Val

Cys Asp Glu Gly Tyr Ile Gly Ala Arg Cys Glu Arg Val Asp Leu 35 40 45

- (2) INFORMATION FOR SEQ ID NO:12:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 46 amino acids
    - (B) TYPE: Amino Acid
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: hEGF.egf
  - (B) LOCATION: 1-46

- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His 1 5 10 15

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys 20 25 30

Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp 35 40 45

Leu 46

- (2) INFORMATION FOR SEQ ID NO:13:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 45 amino acids
    - (B) TYPE: Amino Acid
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: hHB-EGF.egf
  - (B) LOCATION: 1-45
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His 1 5 10 15

Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Ile 20 25 30

Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

- (2) INFORMATION FOR SEQ ID NO:14:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 49 amino acids .
    - (B) TYPE: Amino Acid
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: hHRGalpha.egf
  - (B) LOCATION: 1-49
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
- His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn 1 5 10 15

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Tyr Pro (2) INFORMATION FOR SEQ ID NO:15: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 amino acids (B) TYPE: Amino Acid (D) TOPOLOGY: Linear (ix) FEATURE: (A) NAME/KEY: hHRGbeta.eqf (B) LOCATION: 1-48 (C) IDENTIFICATION METHOD: (D) OTHER INFORMATION: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15: His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val (2) INFORMATION FOR SEQ ID NO:16: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 amino acids (B) TYPE: Amino Acid (D) TOPOLOGY: Linear (ix) FEATURE: (A) NAME/KEY: hTGFalpha.egf (B) LOCATION: 1-45 (C) IDENTIFICATION METHOD:

- (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
- His Phe Asn Asp Cys Pro Asp Ser His Thr Gln Phe Cys Phe His 1 5 10 15
- Gly Thr Cys Arg Phe Leu Val Gln Glu Asp Lys Pro Ala Cys Val 20 25 30

Cys His Ser Gly Tyr Val Gly Ala Arg Cys Glu His Ala Asp Leu 35 40 45

- (2) INFORMATION FOR SEQ ID NO:17:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 45 amino acids
    - (B) TYPE: Amino Acid
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: mEPR.egf
  - (B) LOCATION: 1-45
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
- Gln Ile Thr Lys Cys Ser Ser Asp Met Asp Gly Tyr Cys Leu His 1 5 10 15
- Gly Gln Cys Ile Tyr Leu Val Asp Met Arg Glu Lys Phe Cys Arg 20 25 30
- Cys Glu Val Gly Tyr Thr Gly Leu Arg Cys Glu His Phe Phe Leu
  35 40 45
- (2) INFORMATION FOR SEQ ID NO:18:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 50 amino acids
    - (B) TYPE: Amino Acid
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: Oligonucleotide probe
  - (B) LOCATION: 1-50
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
- Thr Gly Gly Thr Ala Ala Ala Ala Gly Cys Thr Ala Cys Ala Gly  $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$
- Thr Cys Thr Cys Ala Ala Ala Gly Cys Ala Thr Cys Cys Ala Gly 20 25 30
- Cys Ala Cys Ala Ala Thr Gly Gly Cys Ala Ala Ala Gly Thr Cys 35 40 45

Ala Gly Ala Gly Ala

50

- (2) INFORMATION FOR SEQ ID NO:19:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 8 amino acids
    - (B) TYPE: Amino Acid
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: hNRG3B1 transmembrane proximal 1
  - (B) LOCATION: 1-8
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asn Asp Gly Glu Cys Phe Val Ile

- (2) INFORMATION FOR SEQ ID NO:20:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: Amino Acid
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: hNRG3B1 transmembrane proximal 2
  - (B) LOCATION: 1-9
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Glu Phe Met Glu Ser Glu Glu Val Tyr 1 5 9

- (2) INFORMATION FOR SEQ ID NO:21:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 466 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
- (ix) FEATURE:
  - (A) NAME/KEY: EST Genbank entry H23651
  - (B) LOCATION: 1-466
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AATTTCTGCC GAAAACTGAT TCCATCTTAT CGGATCCAAC AGACCACTTG 50
GGGATTGAAT TCATGGAGAG TGAAGAAGTT TATCAAAGGC AGGTGCTGTC 100
AATTTCATGT ATCATCTTTG GAATTGTCAT CGTGGGCATG TTCTGTGCAG 150

CATTCTACTT CAAAAGCAAG AAACAAGCTA AACAAATCCA AGAGCAGCTG 200

AAAGTGCCAC AAAATGGTAA AAGCTACAGT CTCAAAGCAT CCAGCACAAT 250

GGCAAAGTCA GAGAACTTGG TGAAGAGCCA TGTCCAGCTG CAAAATAAAA 300

TGTCAGGCTT CTGAGCCCAA GCTAAGCCAT CATATCCCCT GTNGACCTGC 350

ACGTGCACAT CCNGATGGCC CGTTTCCTGC CTTTTNTGAT GACATTTNCA 400

CCACAAAATGN AGGAG 466

# (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2091 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

#### (ix) FEATURE:

- (A) NAME/KEY: Human NRG3B2 (hNRGB2)
- (B) LOCATION: 1-2091
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGAGTGAAG	GGGCGGCCGC	TGCCTCGCCA	CCTGGTGCCG	CTTCGGCAGC	50
CGCCGCCTCG	GCCGAGGAGG	GCACCGCGGC	GGCTGCGGCG	GCGGCAGCGG	100
CGGGCGGGG	CCCGGACGGC	GGCGGCGAAG	GGGCGGCCGA	GCCCCCCGG	150
GAGTTACGCT	GTAGCGACTG	CATCGTGTGG	AACCGGCAGC	AGACGTGGCT	200
GTGCGTGGTA	CCTCTGTTCA	TCGGCTTCAT	CGGCCTGGGG	CTCAGCCTCA	250
TGCTTCTCAA	ATGGATCGTG	GTGGGCTCCG	TCAAGGAGTA	CGTGCCCACC	300
GACCTAGTGG	ACTCCAAGGG	GATGGGCCAG	GACCCCTTCT	TCCTCTCCAA	350
GCCCAGCTCT	TTCCCCAAGG	CCATGGAGAC	CACCACCACT	ACCACTTCCA	400
CCACGTCCCC	CGCCACCCCC	TCCGCCGGGG	GTGCCGCCTC	CTCCAGGACG	450
CCCAACCGGA	TTAGCACTCG	CCTGACCACC	ATCACGCGGG	CGCCCACTCG	500
CTTCCCCGGG	CACCGGGTGC	CCATCCGGGC	CAGCCCGCGC	TCCACCACAG	550
CACGGAACAC	TGCGGCCCCT	GCGACGGTCC	CGTCCACCAC	GGCCCCGTTC	600
TTCAGTAGCA	GCACGCTGGG	CTCCCGACCC	CCGGTGCCAG	GAACTCCAAG	650
TACCCAGGCA	ATGCCCTCCT	GGCCTACTGC	GGCATACGCT	ACCTCCTCCT	700

ACCTTCACGA TTCTACTCCC TCCTGGACCC TGTCTCCCTT TCAGGATGCT 750 GCCTCCTCTT CTTCCTCTTC TTCCTCCTCC GCTACCACCA CCACACCAGA 800 AACTAGCACC AGCCCCAAAT TTCATACGAC GACATATTCC ACAGAGCGAT 850 CCGAGCACTT CAAACCCTGC CGAGACAAGG ACCTTGCATA CTGTCTCAAT 900 GATGGCGAGT GCTTTGTGAT CGAAACCCTG ACCGGATCCC ATAAACACTG 950 TCGGTGCAAA GAAGGCTACC AAGGAGTCCG TTGTGATCAA TTTCTGCCGA 1000 AAACTGATTC CATCTTATCG GATCCAACAG ACCACTTGGG GATTGAATTC 1050. ATGGAGAGTG AAGAAGTTTA TCAAAGGCAG GTGCTGTCAA TTTCATGTAT 1100 CATCTTTGGA ATTGTCATCG TGGGCATGTT CTGTGCAGCA TTCTACTTCA 1150 AAAGCAAGAA ACAAGCTAAA CAAATCCAAG AGCAGCTGAA AGTGCCACAA 1200 AATGGTAAAA GCTACAGTCT CAAAGCATCC AGCACAATGG CAAAGTCAGA 1250 GAACTTGGTG AAGAGCCATG TCCAGCTGCA AAATTATTCA AAGGTGGAAA' 1300 GGCATCCTGT GACTGCATTG GAGAAAATGA TGGAGTCAAG TTTTGTCGGC 1350 CCCCAGTCAT TCCCTGAGGT CCCTTCTCCT GACAGAGGAA GCCAGTCTGT 1400 CAAACACCAC AGGAGTCTAT CCTCTTGCTG CAGCCCAGGG CAAAGAAGTG 1450 GCATGCTCCA TAGGAATGCC TTCAGAAGGA CACCCCGTC ACCCCGAAGT 1500 AGGCTAGGTG GAATTGTGGG ACCAGCATAT CAGCAACTCG AAGAATCAAG 1550 GATCCCAGAC CAGGATACGA TACCTTGCCA AGGGTATTCA TCCAGTGGTT 1600 TAAAAACCCA ACGAAATACA TCAATAAATA TGCAACTGCC TTCAAGAGAG 1650 ACAAACCCCT ATTTTAATAG CTTGGAGCAA AAGGACCTGG TGGGCTATTC 1700 ATCCACAAGG GCCAGTTCTG TGCCCATCAT CCCTTCAGTG GGTTTAGAGG 1750 AAACCTGCCT GCAAATGCCA GGGATTTCTG AAGTCAAAAG CATCAAATGG 1800 TGCAAAAACT CCTATTCAGC TGACGTTGTC AATGTGAGTA TTCCAGTCAG 1850 CGATTGTCTT ATAGCAGAAC AACAAGAAGT GAAAATATTG CTAGAAACTG 1900 TCCAGGAGCA GATCCGAATT CTGACTGATG CCAGACGGTC AGAAGACTAC 1950 GAACTGGCCA GCGTAGAAAC CGAGGACAGT GCAAGTGAAA ACACAGCCTT 2000 TCTCCCCCTG AGTCCCACAG CCAAATCAGA ACGAGAGGCG CAATTTGTCT 2050 TAAGAAATGA AATACAAAGA GACTCTGCAT TGACCAAGTG A 2091

# (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 696 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

## (ix) FEATURE:

- (A) NAME/KEY: Human NRG3B2
- (B) LOCATION: 1-696
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) S	EQUEN	ICE I	DESC	RIPT	ION:	SEQ	ID	NO:2	3:				
Met Ser 1	Glu	Gly	Ala 5	Ala	Ala	Ala	Ser	Pro 10	Pro	Gly	Ala	Ala	Ser 15
Ala Ala	Ala	Ala	Ser 20	Ala	Glu	Glu	Gly	Thr 25	Ala	Ala	Ala	Ala	Ala 30
Ala Ala	Ala	Ala	Gly 35	Gly	Gly	Pro	Asp	Gly 40	Gly	Gly	Glu	Gly	Ala 45
Ala Glu	Pro	Pro	Arg 50	Glu	Leu	Arg	Cys	Ser 55	Asp	Суз	Ile	Val	Trp 60
Asn Arg	Gln	Gln	Thr 65	Trp	Leu	Cys	Val	Val 70	Pro	Leu	Phe	Ile	Gly 75
Phe Ile	Gly	Leu	Gly 80	Leu	Ser	Leu	Met	Leu 85	Leu	Lys	Trp	Ile	Val 90
Val Gly	Ser	Val	Lys 95	Glu	Tyr	Val	Pro	Thr 10.0	Asp	Leu	Val	Asp	Ser 105
Lys Gly	Met	Gly	Gln 110	Asp	Pro	Phe	Phe	Leu 115	Ser	Lys	Pro	Ser	Ser 120
Phe Pro	Lys	Ala	Met 125	Glu	Thr	Thr	Thr	Thr 130	Thr	Thr	Ser	Thr	Thr 135
Ser Pro	Ala '	Thr	Pro 140	Ser	Ala	Gly	Gly	Ala 145	Ala	Ser	Ser	Arg	Thr 150
Pro Asn	Arg	Ile	Ser 155	Thr	Arg	Leu	Thr	Thr 160	Ile	Thr	Arg	Ala	Pro 165

Thr Arg Phe Pro Gly His Arg Val Pro Ile Arg Ala Ser Pro Arg

Ser Thr Thr Ala Arg Asn Thr Ala Ala Pro Ala Thr Val Pro Ser

Thr Thr Ala Pro Phe Phe Ser Ser Ser Thr Leu Gly Ser Arg Pro

170

185

200

190

205

210

Pro	Val	. Pro	Gly	Thr 215	Pro	Ser	Thr	Gln	Ala 220		Pro	Ser	Trp	Pro 225
Thr	Ala	Ala	Tyr	Ala 230		Ser	Ser	Tyr	Leu 235		Asp	Ser	Thr	Pro 240
Ser	Trp	Thr	Leu	Ser 245		Phe	Gln	Asp	Ala 250	Ala	Ser	Ser	Ser	Ser 255
Ser	Ser	Ser	Ser	Ser 260		Thr	Thr	Thr	Thr 265	Pro	Glu	Thr	Ser	Thr 270
Ser	Pro	Lys	Phe	His 275		Thr	Thr	Tyr	Ser 280	Thr	Glu	Arg	Ser	Glu 285
His	Phe	Lys	Pro	Cys 290	Arg	Asp	Lys	Asp	Leu 295	Ala	Tyr	Cys	Leu	Asn 300
Asp	Gly	Glu	Cys	Phe 305	Val	Ile	Glu	Thr	Leu 310	Thr	Gly	Ser	His	Lys 315
His	Cys	Arg	Cys ·	Lys 320	Glu	Gly	Tyr	Gln	Gly 325	Val	Arg	Cys	Asp	Gln 330
Phe	Leu	Pro	Lys	Thr 335	Asp	Ser	Ile	Leu	Ser 340	Asp	Pro	Thr	Asp	His 345
Leu	Gly	Ile	Glu	Phe 350	Met	Glu	Ser	Glu	Glu 355	Val	Tyr	Gln	Arg	Gln 360
Val	Leu	Ser	Ile	Ser 365	Cys	Ile	Ile	Phe	Gly 370	Ile	Val	Ile	Val	Gly 375
Met	Phe	Cys	Ala	Ala 380	Phe	Tyr	Phe	Lys	Ser 385	Lys	Lys	Gln	Ala	Lys 390
Gln	Ile	Gln	Glu	Gln 395	Leu	Lys	Val	Pro	Gln 400	Asn	Gly	Lys	Ser	Tyr 405
Ser	Leu	Lys	Ala	Ser 410	Ser	Thr	Met	Ala	Lys 415	Ser	Glu	Asn	Leu	Val 420
Lys	Ser	His	Val	Gln 425	Leu	Gln	Asn	Tyr	Ser 430	Lys	Val	Glu	Arg	His 435
Pro '	Val	Thr	Ala	Leu 440	Glu	Lys	Met	Met	Glu 445	Ser	Ser	Phe	Val	Gly 450
Pro (	Gln	Ser	Phe	Pro 455	Glu	Val	Pro	Ser	Pro 460	Asp	Arg	Gly	Ser	Gln 465
Ser V	Val	Lys	His	His 470	Arg	Ser	Leu	Ser	Ser 475	Cys	Cys	Ser	Pro	Gly 480
Gln A	Arg	Ser	Gly	Met 485	Leu	His	Arg	Asn	Ala 490	Phe	Arg	Arg	Thr	Pro 495



Pro	Ser	Pro	Arg	Ser 500	Arg	Leu	Gly	Gly	Ile 505	Val	Gly	Pro	Ala	Tyr 510
Gln	Gln	Leu	Glu	Glu 515	Ser	. Arg	Ile	Pro	Asp 520	Gln	Asp	Thr	Ile	Pro 525
Cys	Gln	Gly	Tyr	Ser 530	Ser	Ser	Gly	Leu	Lys 535	Thr	Gln	Arg	Asn	Thr 540
Ser	Ile	Asn	Met	Gln 545	Leu	Pro	Ser	Arg	Glu 550	Thr	Asn	Pro	Tyr	Phe 555
Asn	Ser	Leu	Glu	Gln 560	Lys	Asp	Leu	Val	Gly 565	Tyr	Ser	Ser	Thr	Arg 570
Ala	Ser	Ser	Val	Pro 575	Ile	Ile	Pro	Ser	Val 580	Gly	Leu	Glu	Glu	Thr 585
Cys	Leu	Gln	Met	Pro 590	Gly	Ile	Ser	Glu	Val 595	Lys	Ser	Ile	Lys	Trp 600
Cys	Lys	Asn	Ser	Tyr 605	Ser	Ala	Asp	Val	Val 610	Asn	Val	Ser	Ile	Pro 615
Val	Ser	Asp	Cys	Leu 620	Ile	Ala	Glu	Gln	Gln 625	Glu	Val	Lys	Ile	Leu 630
Leu	Glu	Thr	Val	Gln 635	Glu	Gln	Ile	Arg	Ile 640	Leu	Thr	Asp	Ala	Arg 645
Arg	Ser	Glu	Asp	Tyr 650	Glu	Leu	Ala	Ser	Val 655	Glu	Thr	Glu	Asp	Ser 660
Ala	Ser	Glu	Asn	Thr 665	Ala	Phe	Leu	Pro	Leu 670	Ser	Pro	Thr	Ala	Lys 675
Ser	Glu	Arg	Glu	Ala 680	Gln	Phe	Val	Leu	Arg 685	Asn	Glu	Ile	Gln	Arg 690
Asp	Ser	Ala	Leu	Thr 695										